Apolipoprotein analogues

The invention relates to a pharmaceutical composition comprising an apolipoprotein construct, to an apolipoprotein construct, a nucleic acid sequence encoding the apolipoprotein construct, a vector comprising the nucleic acid sequence, a method for producing the apolipoprotein construct, and a method of treatment comprising administering the apolipoprotein construct.

Prior art

In the following, the term Apo A or apolipoprotein A will be used to designate any of the three apolipoproteins, Apolipoprotein A I, Apolipoprotein A II, or Apolipoprotein A IV.

Cardiovascular diseases caused by atherosclerosis in the vessels is the most frequent cause of death in the industrialised countries of the World. One of the pathogenic factors causing atherosclerosis is the deposition of cholesterol in the vessel walls leading to plaque formation and eventually to arterosclerosis and increased risk of infarction.

Apolipoprotein A-1 (apo-A-1) is the main component of plasma HDL (high density lipoprotein), which is negatively correlated to the presence of arterosclerosis. There is strong experimental evidence that this effect is caused by so-called reverse cholesterol transport from peripheral tissues to the liver. There is also experimental evidence that this reverse cholesterol transport can be stimulated in mammals by injection of apo-A-1.

Apolipoprotein A-1 is rapidly cleared from plasma. It is believed that Apo-A-1 is to a large extent removed from plasma by filtration in the kidneys without being broken down first (Braschi et al 1999, J Lipid Res, 40:522-532; Braschi et al 2000, Biochemistry, 39:5441-5449; Glass et al 1983, J Biol Chem 258:7161-7167). The short plasma half-life of apolipoprotein A is a constraint against using the protein in the treatment of atherosclerosis.

US 5,876,968 (SIRTORI ET AL.) concerns substantially pure dimers of a variant of apo-A-1 called apolipoprotein A-1-Milano. Medicaments containing the dimer can be used for preventing thrombosis or they can be used as a prodrug for the monomer. A specific feature of this particular variant of apo-A-I is its ability to form covalent dimers with itself. The authors speculated that the presence of Apo A-I-M may be responsible for a prolonged plasma half-life, but no conclusive data have been presented.

US 5,643,757 (SHA-IL ET AL.) discloses a method for the production of pure, stable, mature and biologically active human apolipoprotein A-I in high yield.

US 5,990,081 (AGELAND ET AL.) discloses a method for treatment of arterosclerosis or cardiovascular diseases by administering a therapeutically effective amount of apoliproprotein A or apolipoprotein E.

WO 96/37608 (RHONE-POULENC ROHRER ET AL.) describes human homologous dimers of apolipoprotein A-I variants comprising cystein in position 151. The presence of the cystein residue in the amino acid sequence allows the formation of dimers via disulphide bridges between the monomers. The reference furthermore discloses the corresponding nucleic acid sequences and vectors comprising these as well as pharmaceutical compositions comprising the variants and the use of these in gene therapy.

WO 90/12879 (Sirtori et al) and WO 94/13819 (Kabi Pharmacia) disclose methods for preparation of ApoA-I and ApoA-IM in yeast and E. coli respectively. The documents also disclose the use of ApoA-I and ApoA-IM as a medicament for the treatment of atherosclerosis and cardiovascular diseases.

In conclusion the prior art is mainly concerned with the use of native ApoA-I or ApoA-IM monomer or ApoA-IM dimer as medicaments for the treatment of vascular diseases, despite the known disadvantages of these proteins (mainly rapid clearance). The prior art does not suggest to modify ApoA-I in order to obtain constructs with increased ability to perform reverse cholesterol transport and/or with longer plasma half life. It is thus one object of the present invention to provide such

ApoA constructs, which may be used for treatment and/or prevention of cardiovascular diseases.

Summary

In a first aspect the invention relates to a pharmaceutical composition comprising an apolipoprotein construct having the general formula

- apo A-X,
- where apo A is an apolipoprotein A component selected from the group consisting of apolipoprotein AI, apolipoprotein AII, apolipoprotein AIV, an analogue or a variant thereof,
- and X is a heterologous moiety comprising at least one compound selected from the group consisting of an amino acid, a peptide, a protein, a carbohydrate, and a nucleic acid sequence,
- with the proviso that when the construct consists of exactly two identical, native apolipoproteins these are linked serially.

By the invention is provided a novel pharmaceutical composition. The prior art fails to teach an apoliprotein construct as defined in the present invention for inclusion in a pharmaceutical composition. The apolipoprotein constructs according to the present invention may broadly be looked upon as HDL analogues due to their ability to form complexes with cholesterol and other lipids and assist in the transportation of these compounds to the liver.

Throughout the invention the apolipoprotein component or part of the construct is referred to as apo A or apolipoprotein. In the following and in the claims, the heterologous moiety is referred to as component X of the construct. The apolipoprotein or analogue or variant thereof is linked covalently to the heterologous moiety.

The component X of the construct may be looked broadly upon as a heterologous moiety. In this context a heterologous moiety is any kind of moiety not being linked to apolipoprotein or analogue or variant or functional equivalent thereof under native conditions. The heterologous moiety may thus be a peptide or a protein or part of a peptide or protein from the same or from another species, or even a single amino

acid. It may be a synthetic peptide. It may be of carbohydrate nature or of other polymeric and biocompatible nature such as polyols, nucleic acids sequences.

Functional equivalence to native apolipoprotein A-I, A-II or A-IV may conveniently be measured using a lipid binding assay. The ability of the construct to elicit substantially the same physiological response in a mammal may conveniently be measured by measurement of the ability to perform reverse cholesterol transport in a test organism such as rabbits or rodent such as mice.

The construct comprising apolipoprotein and a heterologous moiety is capable of performing reverse cholesterol transport as well as or even better than native apolipoproteins, despite the modification caused by the addition of a heterologous moiety. The plasma half-life of the construct is preferably increased compared to that of the wild-type apolipoprotein. The increased half-life can be due either to the increased size of the apolipoprotein construct, which may reduce the rate of filtration through the kidneys, it may be due to increased binding to HDL, or it may be due to reduced breakdown of the construct compared to native Apo A.

Preferably the plasma half-life is at least doubled or tripled, or at least quadrupled, or at least 10 doubled. Similarly, the binding affinity such as the lipid binding affinity, and/or the cholesterol binding affinity of the construct is preferably increased as compared to wild-type apolipoprotein. Preferably, the lipid binding affinity is increased by at least 5 %, such as at least 10 %, for example at least 15%, such as at least 20%, for example at least 25%, such as at least 30%, for example at least 40% such as at least 50%, for example at least 75%, such as at least 100%, such as at least 150%, for example at least 200%, such as at least 300%. Even in the cases where the lipid binding affinity of the constructs according to the invention is the same or lower than the lipid binding affinity of native apolipoprotein, the clinical effect may be enhanced due to increased plasma half life of the constructs according to the invention.

An increased plasma half-time and/or increased lipid binding affinity have profound implications for the use of the apolipoprotein constructs in the treatment of arterosclerosis. It is therefore expected that the clinical effect of the apolipoprotein

constructs according to the invention is superior to the effect of wild-type apolipoproteins.

The invention also encompasses analogues or variants of the wild-type apoliproteins capable of eliciting substantially the same physiological response in a mammal.

The pharmaceutical composition may further comprise pharmaceutical acceptable excipients, adjuvants, additives, such as lipids, phospholipids, cholesterol, or triglycerides.

According to a second aspect of the invention, there is provided an apolipoprotein construct having the general formula

- apo A-X,

- where apo A is an apolipoprotein component selected from the group consisting of apolipoprotein AI, apolipoprotein AII, apolipoprotein AIV, an analogue or a variant thereof,

- and X is a heterologous moiety selected from the group consisting of an oligomerising module, and a terminally linked apolipoprotein.

According to a further aspect, there is provided a nucleotide sequence encoding an apolipoprotein construct as defined above. Preferably the nucleotide sequence is operably linked to a regulatory sequence for expression of the protein construct.

According to further aspects of the invention, there is provided a vector comprising the nucleotide sequence encoding the apolipoprotein construct and a transformed host cell comprising the nucleotide sequence as defined above.

The apolipoprotein construct according to the invention may be produced by different methods.

According to a first method a transformed host cell is cultured under conditions promoting the expression of a protein construct according to the invention encoded

by DNA inserted into a construct, obtaining and recovering the protein construct and optionally further processing the protein construct.

This method is the preferred method when the whole construct is of polypeptide nature and thus can be encoded by one corresponding nucleic acid sequence.

According to a second method the apolipoprotein construct can be manufactured by chemically synthesising the heterologous moiety and subsequently linking it to the apolipoprotein or analogue obtaining an apolipoprotein construct, which is isolated and optionally processed further. This method is the preferred method, when the heterologous moiety is of non-peptide nature. However there may also be conditions under which it is preferred to synthesise the heterologous moiety chemically, when it is of polypeptide nature. Such conditions may be that the heterologous moiety is rather short such as below 20 amino acids.

According to a third method the apolipoprotein construct can be manufactured by culturing a transformed host cell under conditions promoting the expression of an apolipoprotein or an apolipoprotein analogue encoded by a nucleic acid fragment and subsequently covalently linking the apolipoprotein or apolipoprotein analogue to a heterologous moiety obtaining an apolipoprotein construct, isolating the resulting apolipoprotein construct and optionally further processing the construct.

Finally, the apolipoprotein construct may be produced by culturing a transformed host cell under conditions promoting the expression of a protein encoded by a nucleic acid fragment encoding an oligomerising module and subsequently linking said module to at least one apolipoprotein obtaining an apolipoprotein construct.

According to a further aspect of the invention there is provided a method for treating a patient having a condition related to cholesterol, phospholipids and triacylglycerides LDL and HDL disorders, and arteriosclerotic diseases comprising administering to the individual a pharmaceutical composition according to the invention.

The pharmaceutical composition may be administered intravenously, intraarterially, intramusculary, transdermally, pulmonary, subcutaneously, intradermally,

intratechally, through the buccal-, anal-, vaginal-, conjunctival-, or intranasal tissue, or by inoculation into tissue, such as tumour tissue, or by an implant, or orally.

The apolipoprotein construct as defined above may also be used for gene therapy, wherein the DNA sequence encoding the apolipoprotein construct is used for transfection or infection of at least one cell population.

Detailed description of the invention

In the following the invention will be described in detail with reference to the following figures.

Figure 1 shows the amino acid sequence (in one letter code) of human apolipoprotein A-I.

Figure 2A shows CLUSTAL W (1.74) multiple sequence alignment of apolipoprotein A-I using BLOSUM. The following sequences are aligned in the Figure:

HUMAN sp|P02647|APA1_HUMAN Apolipoprotein A-I precursor (Apo-AI) - Homo sapiens (Human)

Macaque sp|P15568|APA1_MACFA Apolipoprotein A-I precursor (Apo-AI) - Macaca fascicularis (Crab eating macaque)

Bovine sp|P15497|APA1_BOVIN Apolipoprotein A-I precursor (Apo-AI) - Bos taurus (Bovine).

Pig sp|P18648|APA1_PIG Apolipoprotein A-I precursor (Apo-AI) - Sus scrofa (Pig).

Dog sp|P02648|APA1_CANFA Apolipoprotein A-I precursor (Apo-AI) - Canis familiaris (Dog).

Rabbit sp|P09809|APA1_RABIT Apolipoprotein A-I precursor (Apo-AI) - Oryctolagus cuniculus (Rabbit).

Tree shreew sp|O18759|APA1_TUPGB Apolipoprotein A-I precursor (Apo-AI) - Tupaia glis belangeri (Common tree shrew).

Mouse sp|Q00623|APA1_MOUSE Apolipoprotein A-I precursor (Apo-AI) - Mus musculus (Mouse).

Rat sp|P04639|APA1_RAT Apolipoprotein A-I precursor (Apo-AI) - Rattus norvegicus (Rat).

Eur. Hedgehog tr|Q9TS49 APOLIPOPROTEIN A-I, APOA-I=CHOLESTEROL TRANSPORTER - Erinaceus europaeus (Western European hedgehog).

Chicken sp|P08250|APA1_CHICK Apolipoprotein A-I precursor (Apo-AI) - Gallus gallus (Chicken).

Jap. quail sp|P32918|APA1_COTJA Apolipoprotein A-I precursor (Apo-AI) - Coturnix coturnix japonica (Japanese quail).

Domestic duck sp|O42296|APA1_ANAPL Apolipoprotein A-I precursor (Apo-AI) - Anas platyrhynchos (Domestic duck).

Rainbow trout sp|O57523|AP11_ONCMY Apolipoprotein A-I-1 precursor (APOA-I-1) - Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

Brown trout sp|Q91488|APA1_SALTR Apolipoprotein A-I precursor (Apo-AI) - Salmo trutta (Brown trout).

Atl. salmon sp|P27007|APA1_SALSA Apolipoprotein A-I precursor (Apo-AI) - Salmo salar (Atlantic salmon).

Zebrafish sp|O42363|APA1_BRARE Apolipoprotein A-I precursor (Apo-AI) - Brachydanio rerio (Zebrafish) (Zebra danio).

Sea bream sp|O42175|APA1_SPAAU Apolipoprotein A-I precursor (Apo-AI) - Sparus aurata (Gilthead sea bream).

Figure 2B shows aligned amino acid sequences (in one letter code) for human, macaque, mouse, baboon, pig, and rat apolipoprotein A-IV.

Figure 3: Amino acid sequence of the amino terminal region of tetranectin (SEQ ID NO 12). Amino acid sequence (in one letter code) from El to L51 of tetranectin. Exon 1 comprises residues El to D16 and exon 2 residues V17 to V49, respectively. The alpha helix extends beyond L51 to K52 which is the C-terminal amino acid residue in the alpha helix.

Figure 4 shows an alignment of the amino acid sequences of the trimerising structural element of the tetranectin protein family. Amino acid sequences (one letter code) corresponding to residue V17 to K52 comprising exon 2 and the first three residues of exon 3 of human tetranectin; murine tetranectin (Sørensen et al., Gene, 152: 243 -245, 1995); tetranectin homologous protein isolated from reefshark cartilage (Neame and Boynton, 1992,1996); and tetranectin homologous protein isolated from bovine cartilage (Neame and Boynton, database accession number PATCHX:u22298). Residues at a and d positions in the heptad repeats are listed in boldface. The listed consensus sequence of the tetranectin protein family trimerising structural element comprise the residues present at a and d positions in the heptad repeats shown in the figure in addition to the other conserved residues of the region. "hy" denotes an aliphatic hydrophobic residue.

Figure 5 shows the pT7 H6UbiFx Apo A-I plasmid and its corresponding amino acid sequences. The expressed and processed polypeptide consists of amino acids no 25-267 from human Apo A-I (SEQ ID NO 1) and gly-gly linked N-terminally thereto.

Figure 6 shows the pT7 H6UbiFx Cys-Apo A-I plasmid and its corresponding amino acid sequences for. The expressed and processed polypeptide consists of a N-terminal cystein residue and the amino acids no 25-267 from human Apo A-I (SEQ ID NO 2) and gly-gly linked N-terminally thereto.

Figure 7 shows the pT7H6 Trip-A-Apo A-I - Amp^R plasmid and its corresponding amino acid sequence. The expressed and processed polypeptide (SEQ ID NO 3)

consists of the TTSE, a linking sequence, and amino acids no 25-267 from human Apo A-I.

Figure 8 shows the pT7H6 Trip-A-Apo A-I-del 43 - Amp^R plasmid and its corresponding amino acid sequence. The expressed and processed polypeptide (SEQ ID NO 4) consists of the TTSE, a linking sequence, and amino acids no 68-267 from human Apo A-I.

Figure 9 shows the pT7H6FXCysApoAI plasmid and its corresponding amino acid sequence. The expressed and processed polypeptide consists of a N-terminal cystein residue and the amino acids no 25-267 from human Apo A-I (SEQ ID NO 2) and gly-gly linked N-terminally thereto.

Figure 10 A to G shows illustrative examples of plasmids and corresponding amino acid sequences for apolipoprotein constructs according to the present invention.

Fig 10 A: pT7H6-Trip-A-Apo AI K9A K15A: Corresponds to pT7H6-Trip-A-Apo AI but two lysine residues in the trimerisation region has been mutated to remove the heparin affinity. The mature protein product is called Trip-A-AI K9A,K15A (SEQ ID NO 5).

Fig 10 B: pT7H6 Trip-A-FN-Apo AI: Corresponds to pT7H6-Trip-A-Apo AI, however, bases encoding the amino acid sequence SGH has been inserted after the Trip A sequence and before the apo AI sequence. The mature protein product is named Trip-A-FN-AI (SEQ ID NO 6).

Fig 10 C: pT7H6 Trip-A-FN-Apo AI-final: Corresponds to pT7H6 Trip-A-FN-Apo AI, however, the BamHI site of pT7H6 Trip-A-FN-Apo AI has been removed and the inserted three amino acid sequence changed, so that the amino acid sequence between the tetranectin derived trimerisation sequence and apo AI has been changed from GSSGH to GTSGQ. The five amino acid sequence corresponds to a sequence in the linker region of fibronectin. The mature protein product is named Trip-A-FN-AI-final (SEQ ID NO 7).

Fig 10 D: pT7H6 Trip-A-FN-Apo AI-final K9AK15A: Corresponds to pT7H6-Trip-A-FN-Apo AI-final but two lysine residues in the trimerisation region has been mutated to remove the heparin affinity. The mature protein product is called Trip-A-FN-AI-final-K9A,K15A (SEQ ID NO 8).

Fig 10 E: pT7H6 Trip-A-TN-Apo AI: Corresponds to pT7H6-Trip-A-Apo AI, however, bases encoding the amino acid sequence KVHMK has been inserted after the Trip A sequence and before the apo AI sequence. The mature protein product is named Trip-A-TN-AI (SEQ ID NO 9).

Fig 10 F: pT7H6 Trip-A-TN-Apo AI-final: Corresponds to pT7H6 Trip-A-TN-Apo AI, however, the BamHI site of pT7H6 Trip-A-TN-Apo AI has been removed so that the amino acid sequence between the tetranectin derived trimerisation sequence and apo AI has been changed from GSKVHMK to GTKVHMK. The seven amino acid sequence corresponds to the sequence of tetranectin following the trimerisation domain. The mature protein product is named Trip-A-TN-AI-final (SEQ ID NO 10).

Fig 10 G: pT7H6 Trip-A-TN-Apo AI-final K9AK15A: Corresponds to pT7H6-Trip-A-TN-Apo AI-final but two lysine residues in the trimerisation region has been mutated to remove the heparin affinity. The mature protein product is called Trip-A-TN-AI-final-K9A,K15A (SEQ ID NO 11).

Fig 10 H: pT7H6Fx-Hp(alpha)-ApoAI. The plasmid codes for the fusion protein between Hp(alpha) and ApoAi. The mature protein product is called Hp(alpha)-ApoAI (SEQ ID NO 14).

Figure 11 shows the result of binding of ApoA-I, TripA-ApoA-I, and TripA-FN-ApoA-I to DMPC in the assay described in Example 6.

Figure 12 shows binding of ApoA-I and TripA-ApoA-I to immobilised cubilin as described in Example 7.

Figure 13 shows analytical gelfiltration of Apo A-I, Trip-A-AI, Trip-A-TN-AI, Trip-A-FN-AI. As controls BSA was included. Details are disclosed in Example 5.

Figure 14 shows the results of the evaluation of plasma clearance of apolipoprotein A-I, TripA Apo-AI, and TripA-fibronectin-linker Apo A-I in mice. Experimental details can be found in Example 8.

Detailed description of the invention

The functionality of the constructs according to the invention and of the apo-A components of the constructs can be measured by a lipid binding assay such as by the DPMC assay described below. Furthermore, the in vivo effect on reverse cholesterol transport may be measured by administration to test animals such as rabbits fed on a cholesterol rich diet such as the method disclosed in Miyazaki et al (Arteriosclerosis, Thrombosis, and Vascular Biology, 1995; 15:1882-1888) or in Apo E deficient mice (Sha PK et al, Circulation 2001, 103:3047-3050).

The apolipoprotein or analogue

In the following the term "apo-A" is used to designate any apolipoprotein A comprising apolipoprotein A-I, apolipoprotein A-II or apolipoprotein A-IV, any variant or analogue thereof possessing the same lipid binding function.

Preferred apolipoprotein A-I analogues include those disclosed in Figure 2A. Preferred apolipoprotein A-IV analogues include those disclosed in Figure 2B.

Known variants of the sequences of human Apo-AI in Figure 1 include the following variants, indicating the position of the variation with respect to the sequence in Figure 1, the variation, and where appropriate the name of the known variant.

27 P -> H (IN MUNSTER-3C).
27 P -> R.
28 P -> R (IN MUNSTER-3B).
34 R -> L (IN BALTIMORE).
50 G -> R (IN IOWA).
84 L -> R (IN AUTOSOMAL DOMINANT AMYLOIDOSIS).
113 D -> E.
119 A -> D (IN HITA).
127 D -> N (IN MUNSTER-3A).

131 MISSING (IN MARBURG/MUNSTER-2).
131 K -> M.
132 W -> R (IN TSUSHIMA).
133 E -> K (IN FUKUOKA).
151 R->C (PARIS)
160 E -> K (IN NORWAY).
163 E -> G.
167 P -> R (IN GIESSEN).
168 L -> R (IN ZARAGOZA).
171 E -> V.
189 P -> R.
197 R -> C (IN MILANO).
222 E -> K (IN MUNSTER-4).

According to the invention the term "apolipoprotein" is meant to include functional equivalents of at least one sequence in Figure 1, 2a and 2b, or a fragment of at least one sequence in Figure 1, 2a and 2b, comprising a predetermined amino acid sequence. A "fragment" is defined as:

i) fragments comprising an amino acid sequence capable of being recognised by an antibody also capable of recognising the predetermined amino acid sequences in Figure 1, 2a or 2b, and/or

ii) fragments comprising an amino acid sequence capable of binding to a lipid such as dimyristoyl phosphatidylcholine or cholesterol, and/or a receptor, which is also capable of binding the predetermined amino acid sequences in Figure 1, 2a or 2b.

According to the present invention a functional equivalent of an apolipoprotein or fragments thereof may be obtained by addition, substitution or deletion of at least one amino acid. When the amino acid sequence comprises a substitution of one amino acid for another, such a substitution may be a conservative amino acid substitution. Fragments of the sequences in Figure 1, 2a and 2b may comprise more than one such substitution, such as e.g. two conservative amino acid substitutions, for example three or four conservative amino acid substitutions, such as five or six

conservative amino acid substitutions, for example seven or eight conservative amino acid substitutions, such as from 10 to 15 conservative amino acid substitutions, for example from 15 to 25 conservative amino acid substitution, such as from 25 to 75 conservative amino acid substitutions, for example from 75 to 125 conservative amino acid substitutions, such as from 125 to 175 conservative amino acid substitutions. Substitutions can be made within any one or more groups of predetermined amino acids.

Examples of fragments comprising one or more conservative amino acid substitutions including one or more conservative amino acid substitutions within the same group of predetermined amino acids, or a plurality of conservative amino acid substitutions, wherein each conservative substitution is generated by substitution within a different group of predetermined amino acids.

Accordingly, a variant of the sequences in Figure 1, 2a or 2b, or fragments thereof according to the invention may comprise, within the same variant of the sequences in Figure 1, 2a or 2b, or fragments thereof or among different variant of the sequences in Figure 1, 2a or 2b, or fragments thereof, at least one substitution, such as a plurality of substitutions introduced independently of one another. Variants of the sequences in Figure 1, 2a or 2b, or fragments thereof may thus comprise conservative substitutions independently of one another, wherein at least one glycine (Gly) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof of the sequences in Figure 1, 2a or 2b is substituted with an amino acid selected from the group of amino acids consisting of Ala, Val, Leu, and Ile, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one of said alanines (Ala) of said variant of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Gly, Val, Leu, and Ile, and independently thereof, variant of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one valine (Val) of said variant of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Gly, Ala, Leu, and Ile, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one of said leucines (Leu) of said variant of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of

amino acids consisting of Gly, Ala, Val, and Ile, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one isoleucine (Ile) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Gly, Ala, Val and Leu, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof wherein at least one of said aspartic acids (Asp) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Glu, Asn, and Gln, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one of said phenylalanines (Phe) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Tyr, Trp, His, Pro, and preferably selected from the group of amino acids consisting of Tyr and Trp, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one of said tyrosines (Tyr) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof of the sequences in Figure 1, 2a or 2b is substituted with an amino acid selected from the group of amino acids consisting of Phe, Trp, His, Pro, preferably an amino acid selected from the group of amino acids consisting of Phe and Trp, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one of said arginines (Arg) of said fragment of the sequences in Figure 1, 2a or 2b is substituted with an amino acid selected from the group of amino acids consisting of Lys and His, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one lysine (Lys) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Arg and His, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one of said aspargines (Asn) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Asp, Glu, and Gln, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one glutamine (Gln) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Asp, Glu, and Asn, and independently thereof, variants of the

sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one proline (Pro) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Phe, Tyr, Trp, and His, and independently thereof, variants of the sequences in Figure 1, 2a or 2b, or fragments thereof, wherein at least one of said cysteines (Cys) of said variants of the sequences in Figure 1, 2a or 2b, or fragments thereof is substituted with an amino acid selected from the group of amino acids consisting of Asp, Glu, Lys, Arg, His, Asn, Gln, Ser, Thr, and Tyr.

It is clear from the above outline that the same variant or fragment thereof may comprise more than one conservative amino acid substitution from more than one group of conservative amino acids as defined herein above.

The addition or deletion of an amino acid may be an addition or deletion of from 2 to 10 amino acids, such as from 10 to 20 amino acids, for example from 20 to 30 amino acids, such as from 40 to 50 amino acids. However, additions or deletions of more than 50 amino acids, such as additions from 10 to 200 amino acids, are also comprised within the present invention. More specifically, 43 N-terminal amino acids may be removed from the sequence in Figure 1 without substantially altering the lipid binding effect of the protein. Such a deletion variant is included in SEQ ID NO 4 as the apolipoprotein part of the construct.

It will thus be understood that the invention concerns apolipoproteins comprising at least one fragment of the sequences in Figure 1, 2a or 2b capable of binding lipids such as DPMC, including any variants and functional equivalents of such at least one fragment.

The apolipoprotein according to the present invention, including any functional equivalents and fragments thereof, may in one embodiment comprise less than 243 amino acid residues, such as less than 240 amino acid residues, for example less than 225 amino acid residues, such as less than 200 amino acid residues, for example less than 180 amino acid residues, such as less than 160 amino acid residues, for example less than 150 amino acid residues, such as less than 140 amino acid residues, for example less than 130 amino acid residues, such as less than 120 amino acid residues, for example less than 110 amino acid residues, such

as less than 100 amino acid residues, for example less than 90 amino acid residues, such as less than 85 amino acid residues, for example less than 80 amino acid residues, such as less than 75 amino acid residues, for example less than 70 amino acid residues, such as less than 65 amino acid residues, for example less than 60 amino acid residues, such as less than 55 amino acid residues, for example less than 50 amino acid residues.

Fragments

A fragment comprising the lipid binding region of the native sequences in Figure 1, 2a or 2b is particularly preferred. However, the invention is not limited to fragments comprising the lipid binding region. Deletions of such fragments generating functionally equivalent fragments of the sequences in Figure 1, 2a or 2b comprising less than the lipid binding region are also comprised in the present invention. Functionally equivalent the sequences in Figure 1, 2a or 2b peptides, and fragments thereof according to the present invention, may comprise less or more amino acid residues than the lipid binding region. Preferably, the fragment comprises at least the amino acids 100-186 of apo-A-I or a variant or a functional equivalent thereof. It has been determined that this central domain and the α-helices within the domain are directly involved in interactions with phospholipids. Therefore, it is highly likely that this region plays an important role in the functional properties of apo-A-I.

"Functional equivalency" as used in the present invention is according to one preferred embodiment established by means of reference to the corresponding functionality of a predetermined fragment of the sequences in Figure 1, 2a or 2b.

Functional equivalents of variants of the sequences in Figure 1, 2a or 2b will be understood to exhibit amino acid sequences gradually differing from the preferred predetermined sequence, as the number and scope of insertions, deletions and substitutions including conservative substitutions increases. This difference is measured as a reduction in homology between the preferred predetermined sequence and the fragment or functional equivalent.

All fragments or functional equivalents of apolipoprotein are included within the scope of this invention, regardless of the degree of homology that they show to a

preferred predetermined sequence of apolipoprotein. The reason for this is that some regions of the sequences in Figure 1, 2a or 2b are most likely readily mutatable, or capable of being completely deleted, without any significant effect on the binding activity of the resulting fragment.

A functional variant obtained by substitution may well exhibit some form or degree of native activity of the sequences in Figure 1, 2a or 2b, and yet be less homologous, if residues containing functionally similar amino acid side chains are substituted. Functionally similar in this respect refers to dominant characteristics of the side chains such as hydrophobic, basic, neutral or acidic, or the presence or absence of steric bulk. Accordingly, in one embodiment of the invention, the degree of identity between i) a given the sequences in Figure 1, 2a or 2b fragment capable of effect and ii) a preferred predetermined fragment, is not a principal measure of the fragment as a variant or functional equivalent of a preferred predetermined the sequences in Figure 1, 2a or 2b fragment according to the present invention.

The homology between amino acid sequences may be calculated using well known algorithms such as BLOSUM 30, BLOSUM 40, BLOSUM 45, BLOSUM 50, BLOSUM 55, BLOSUM 60, BLOSUM 62, BLOSUM 65, BLOSUM 70, BLOSUM 75, BLOSUM 80, BLOSUM 85, or BLOSUM 90. Preferably the algorithm BLOSUM 30 is used.

Fragments sharing at least some homology with the sequences in Figure 1, 2a or 2b fragment are to be considered as falling within the scope of the present invention when they are at least about 40 percent homologous with the apolipoprotein or fragment thereof, such as at least about 50 percent homologous, for example at least about 60 percent homologous, such as at least about 70 percent homologous, for example at least about 75 percent homologous, such as at least about 80 percent homologous, for example at least about 85 percent homologous, such as at least about 90 percent homologous, for example at least 92 percent homologous, such as at least 94 percent homologous, for example at least 95 percent homologous, such as at least 96 percent homologous, for example at least 97 percent homologous, such as at least 98 percent homologous, for example at least 99 percent homologous with the sequences in Figure 1, 2a or 2b fragment.

According to one embodiment of the invention the homology percentages refer to identity percentages.

Additional factors that may be taken into consideration when determining functional equivalence according to the meaning used herein are i) the ability of antisera against one of the sequences in Figure 1, 2a or 2b to detect fragments of the sequences in Figure 1, 2a or 2b according to the present invention, or ii) the ability of the functionally equivalent fragment to compete with the sequences in Figure 1, 2a or 2b in a lipid binding assay.

Conservative substitutions may be introduced in any position of a preferred predetermined apolipoprotein or fragment thereof. It may however also be desirable to introduce non-conservative substitutions, particularly, but not limited to, a non-conservative substitution in any one or more positions.

A non-conservative substitution leading to the formation of a functionally equivalent fragment of the sequences in Figure 1, 2a or 2b would for example i) differ substantially in polarity, for example a residue with a non-polar side chain (Ala, Leu, Pro, Trp, Val, Ile, Leu, Phe or Met) substituted for a residue with a polar side chain such as Gly, Ser, Thr, Cys, Tyr, Asn, or Gln or a charged amino acid such as Asp, Glu, Arg, or Lys, or substituting a charged or a polar residue for a non-polar one; and/or ii) differ substantially in its effect on polypeptide backbone orientation such as substitution of or for Pro or Gly by another residue; and/or iii) differ substantially in electric charge, for example substitution of a negatively charged residue such as Glu or Asp for a positively charged residue such as Lys, His or Arg (and vice versa); and/or iv) differ substantially in steric bulk, for example substitution of a bulky residue such as His, Trp, Phe or Tyr for one having a minor side chain, e.g. Ala, Gly or Ser (and vice versa).

Substitution of amino acids may in one embodiment be made based upon their hydrophobicity and hydrophilicity values and the relative similarity of the amino acid side-chain substituents, including charge, size, and the like. Exemplary amino acid substitutions which take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate

and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition to the variants described herein, sterically similar variants may be formulated to mimic the key portions of the variant structure and that such compounds may also be used in the same manner as the variants of the invention. This may be achieved by techniques of modelling and chemical designing known to those of skill in the art. It will be understood that all such sterically similar constructs fall within the scope of the present invention.

The component X

Preferably, the component X of the protein construct according to the invention is essentially non-immunogenic. For instance the component X may be an amino acid, a carbohydrate, a nucleic acid sequence, an inert protein or polypeptide, which has substantially no physiological effect and especially no immunological effect on mammals.

Preferably the component X is non inmmunogenic and does not interfere negatively with regard to ligand binding, i.e. the apolipoprotein component should not be directed at an undesired site through interactions of the X-component with a ligand.

According to one embodiment the component X consists of just one amino acid, which amino acid preferably is a cystein residue, which may be placed N-terminally, C-terminally or internally in the apolipoprotein component. Such a construct may form a dimer with other identical or similar constructs. Preferably a linker is introduced between the terminal cystein residue and the apolipoprotein component to facilitate the correct folding and lipid interaction of the construct.

However, more preferably the component X comprises a peptide having more than 1 amino acids such as more than 2 amino acids, for example more than 5 amino acids, such as more than 10 amino acids, for example more than 15 amino acids, such as more than 20 amino acids, such as more than 30 amino acids, for example more than 40 amino acids, such as more than 50 amino acids, for example more than 75 amino acids, such as more than 100 amino acids, for example more than

200 amino acids, such as more than 300 amino acids, for example more than 400 amino acids, such as more than 500 amino acids, for example more than 600 amino acids, such as more than 700 amino acids, for example more than 800 amino acids, such as more than 900 amino acids, for example more than 1000, 1250, 1500, 2000, or 2500 amino acids.

In the case where the X-component is a protein, this protein is preferably a mammalian protein and more preferably a human protein. Examples of suitable proteins include plasma proteins such as albumin or serum albumin or another non-immunogenic peptide or protein such as the serine protease fragment of plasminogen or another serine protease engineered to be inactive by disruption of the catalytic triad; and the constant region of the heavy chain of immunoglobins. More preferably, the protein comprises serum albumin. Even more preferably the protein comprises an apolipoprotein containing an amphipatic helix containing apolipoprotein.

According to an especially preferred embodiment of the invention, the component X comprises an apolipoprotein component selected from the group consisting of apolipoprotein A-I, A-II, AIV, an analogue, functional variant or fragment thereof. The two apolipoprotein components may be linked linearly or they may be linked via an additional non-native terminal cystein bridge.

Higher oligomers as well as dimers of the apolipoprotein component comprising at least one non-native cystein residue may be manufactured and linked through cystein bridges under appropriate conditions. Oligomers linked by disulphide bridges may be linked serially (apo-A-S-S-apo-A, or apo-A-S-S-apo-A-S-S-apo-A or higher oligomers).

The protein construct according to the invention may also comprise two, three or more apolipoproteins or analogues thereof being serially and covalently linked to one another. This may be achieved by linking the C-terminal of a first apolipoprotein to the N-terminus of the next apolipoprotein and so forth. The proteins may be so linked after transcription and translation or the nucleotide sequence may simply comprise two, three or more sequences coding for the apolipoprotein construct in question as well as optional linker peptides between the apolipoproteins.

Thereby, the need for a heterologous moiety to perform the linkage is avoided. It is expected that in the constructs having two, three or more apo-A units essentially all the apo-A units will participate in lipid binding thereby contributing to the functionality of the construct. Therefore it is expected that these multi-apo-A constructs have an increased lipid binding ability compared to native apo-A. An additional advantage of these constructs compared to native apo-A, is that they have an increased plasma half-life compared to native apo-A.

Such constructs comprising more than one apolipoprotein component may comprise a combination selected from the following group:

Dimers:
A-I A-I; A-II AII; A-IV A-IV; A-I A-II; A-I A-IV; A-II A-IV.

Trimers:
A-I A-II A-IV; A-I A-I A-II; A-I A-I A-I; A-I A-I A-IV; A-II A-II A-I; A-II A-II A-IV; A-II A-II A-II; A-IV A-IV A-IV; A-IV A-IV A-II; A-IV A-IV A-I.

Oligomerisation modules

According to an especially preferred embodiment of the invention, the heterologous moiety is an oligomerising module. In this context, an oligomerising module is a peptide or a protein or part of a protein which is capable of interacting with other, similar or identical oligomerising modules. The interaction is of the type that produces multimeric proteins or polypeptides. Such an interaction may be caused by covalent bonds between the components of the multimer as well as by hydrogen bond forces, hydrophobic forces, van der Waals forces, salt bridges. The invention also encompasses oligomerising modules of non-peptide nature such as a nucleic acid sequence of DNA, RNA, LNA, or PNA. The skilled person is familiar with techniques to link proteins and nucleic acid sequences to one another.

The oligomerisation module may be a dimerising module, a trimerising module, a tetramerising module, or a multimerising module.

When the apolipoprotein or analogue part of the construct is coupled to an oligomerising module, multimers of the construct can be made by simply mixing a solution of constructs (oligomerisation module linked to apolipoprotein part) under appropriate conditions. In this way, dimers, trimers, tretramers, pentamers, hexamers or higher –mers can be made depending on the type of oligomerising module being linked to the apolipoprotein part of the construct.

The multimers according to the invention may be homomers or heteromers, since different apolipoproteins can be linked to the oligomerising modules and be incorporated into the multimer. It may be advantageous to mix the different types of apolipoproteins in this way to obtain an improved clinical effect of the construct. Preferred homomers include trimers of Apo-A-I and trimers of Apo-A-IV.

According to an especially preferred embodiment of the invention the oligomerising module is from tetranectin and more specifically comprises the tetranectin trimerising structural element (hereafter termed TTSE, SEQ ID NO 12), which is described in detail in WO 98/56906. The amino acid sequence of TTSE is set forth in SEQ ID NO 12. The trimerising effect of TTSE is caused by a coiled coil structure which interacts with the coiled coil structure of two other TTSEs to form a trimer, which is exceptionally stable. A further advantage of TTSE is that it is a weak antigen (WO 98/56906).

Preferably the heparin binding site, which is located in the N-terminal region of exon 1 (Figure 4) is abolished by removal or mutagenis of N-terminal lysine residues (residues 9 and 14 of SEQ ID NO 12) (Nielsen et al, 1997, FEBS Lett 412:388-396) without inhibiting trimerisation. Preferably the lysine residues are mutagenised to alanine. TTSEs that include most or all of exon 1 therefore confer an affinity for sulfated polysaccharides to any designed protein which encompasses such a TTSE as part of its structure. If desired, however, this affinity can be reduced or abolished by N-terminal truncation or mutagenesis of lysine residues in the part of the TTSE that corresponds to the N-terminal amino acid residues of tetranectin (Lorentsen et al 2000, Biochem J 347:83-87).

The interacting domain of the trimerising module according to the invention is preferably of the same type as in TTSE, namely a triple alpha helical coiled coil.

The TTSE may be from human tetranectin, from rabbit tetranectin, from murine tetranectin or from C-type lectin of shark cartilage. Preferably, the TTSE comprises a sequence having at least 68%, such as at least 75%, for example at least 81%, for example at least 87% such as at least 92% identity with the consensus sequence of SEQ ID NO 12. Thereby analogues of the TTSE having substantially the same trimerising effect are encompassed by the invention.

Preferably, the cystein residue 50 of TTSE (SEQ ID NO 12) should be mutagenised to serine, threonine, methionine or to any other amino acid residue in order to avoid formation of an unwanted inter-chain disulphide bridge, which could lead to unwanted multimerisation.

The presence of a trimer may be ascertained by well known techniques such as gel-filtration, SDS-PAGE, or native SDS gel electrophoresis depending on the nature of the trimer. One preferred method for ascertaining the presence of an oligomer is through linkage by DMSI (dimethylsubirimidate) followed by SDS-PAGE.

According to a preferred embodiment of the invention the protein construct is obtained by linking two or more apolipoproteins to oligomerising modules. The advantage of this embodiment is that the linkage of the individual apolipoproteins to one another does not take place within the apolipoprotein but in the oligomerising module. Thereby the nature of the wild-type apolipoprotein is conserved and the apolipoprotein conserves the secondary and tertiary structure, which is advantageous for its physiological function. By further introducing a peptide spacer between the apolipoprotein and the oligomerising module it is ensured that both of the components of the construct can perform their interaction with lipids and other oligomerising modules respectively without being affected by the interactions of the other component. Preferably, the peptide spacer is non-immunogenic, and has an essentially linear three dimensional structure.

Different or identical apo-A units may be oligomerised using an oligomerisation module such as a dimerising module, a trimerising module, a tetramerising module, a pentamerising module, a hexamerising module or a multimerising module. The oligomerising modules may comprise a coiled coil structure capable of interchain recognition and interaction.

The general method for producing an artificial trimer of a protein or peptide comprises the identification of a trimerisation module from proteins that form trimers in nature. Through careful analysis, the domain responsible for the protein-protein interaction can be identified, isolated, and linked to the protein or peptide to be trimerised. According to the invention such trimerisation does not necessarily comprise the formation of a trimer of apolipoprotein or an analogue. It is also possible to link just one apolipoprotein to a trimerisation module and allow this peptide to trimerise with two other trimerisation modules. Thereby the molecular weight of the apolipoprotein part is increased and the plama half-life may be increased compared to native apolipoprotein.

One example of an oligomerisation module is disclosed in WO 95/31540 (HOPPE ET AL.), which describes polypeptides comprising a collectin neck region. The amino acid sequence constituting the collectin neck region may be attached to any polypeptide of choice. Trimers can then be made under appropriate conditions between three polypeptides comprising the collectin neck region amino acid sequence.

Another example of an oligomerisation module is the α1-chain from Haptoglobin. The α1-chain has a cystein residue which may link to another α1-chain to form a dimer. A natural variant is the α2-chain, which has had part of the α1-chain involved in disulphide bridging duplicated. The α2-chain may form cystein bridges to cystein residues in other α2 or α1-chains thereby forming trimers, tetramers, pentamers, hexamers and higher -mers. In the natural form the α-chain is associated to a β-chain. It is possible to replace the β-chain with an apolipoprotein to make an apo-A-α-chain (haptoglobin) construct.

Spacer peptide

The protein construct may also advantageously comprise a spacer moiety, which is covalently linked between the apolipoprotein or apolipoprotein analogue and the heterologous moiety. The effect of the spacer is to provide space between the heterologous moiety and the apolipoprotein part of the construct. Thereby is ensured that the secondary structure of the apolipoprotein part is not affected by the

presence of the heterologous moiety so that the physiological effect of the apolipoprotein part is maintained. Preferably, the spacer is of polypeptide nature. In this way the nucleic acid sequence encoding the spacer can be linked to the sequence encoding the apolipoprotein part of the construct and optionally the sequence for the heterologous moiety, and the whole construct can be produced at the same time.

Design and preparation of suitable spacer moieties are known in the art and are conveniently effected by preparing fusion polypeptides having the format apo-A-spacer-X, where the spacer moiety is a polypeptide fragment (often a relatively inert one), so as to avoid undesired reactions between the spacer and the surroundings or the construct.

A spacer moiety may also be inserted between two TTSEs allowing both of these to interact with a third separate TTSE to form a trimeric complex, which then comprises two separate peptides: TTSE and TTSE-spacer-TTSE. This embodiment facilitates the production of the apolipoprotein construct since the major part of the trimer, which is then strictly seen a dimer, can be synthesised as one single polypeptide comprising in the fusion partners (apo-A denoting any polypeptide sequence forming the apolipoprotein part of the construct) apo-A-TTSE-spacer-TTSE-apo-A.

In the embodiments where two TTSEs are present in the same monomer it is preferred that the spacer moiety has a length and a conformation which favours complex formation involving both of the two TTSEs which are covalently linked by the spacer moiety. In this way, problems arising from undesired formation of trimers of the formats (2+1+1), (2+2+2), and (2+2+1) (wherein only one TTSE of each monomer participates in complex formation) can be diminished.

The spacer peptide preferably comprises at least two amino acids, such as at least three amino acids, for example at least five amino acids, such as at least ten amino acids, for example at least 15 amino acids, such as at least 20 amino acids, for example at least 30 amino acids, such as at least 40 amino acids, for example at least 50 amino acids, such as at least 60 amino acids, for example at least 70 amino acids, such as at least 80 amino acids, such as at least 90 amino acids such as approximately 100 amino acids.

The spacer may be linked to the apo-A component and X through covalent linkages. and preferably the spacer is essentially non-immunogenic, and/or is not prone to proteolytic cleavage, and/or does not comprise any cystein residues.

Similarly, the three-dimensional structure of the spacer is preferably linear or substantially linear.

The following are examples of spacer sequences, which are believed to be especially preferable for linking apolipoprotein analogues to a component X. Preferred examples of spacer or linker peptides include those, which have been used to link proteins without substantially impairing the function of the linked proteins or at least without substantially impairing the function of one of the linked proteins. More preferably the linkers or spacers have been used to link proteins comprising coiled-coil structures.

Tetranectin based linker:

The linker may include the tetranectin residues 53-56, which in tetranectin forms a β-strand, and the residues 57-59 which forms a turn in tetranectin (Nielsen BB, Kastrup JS, Rasmussen H, Holtet TL, Graversen JH, Etzerodt M, Thøgersen HC, Larsen IK, FEBS-Letter 412, 388-396, 1997). The sequence of the segment is GTKVHMK. This linker has the advantage that it in native tetranectin is bridging the trimerisation domain with the CRD-domain, and hence is imagined to be well suited for connecting the trimerisation domain to another domain in general. Furthermore the resulting construct is not expected to be more immunogenic than the construct without a linker. The tetranectin based linker is highly preferred when the component X comprises the TTSE.

Fibronectin based linker:

The linker may be chosen as a sub-sequence from the connecting strand 3 from human fibronectin, this corresponds to amino acid residues 1992-2102 (SWISS-PROT numbering, entry P02751). Preferably the subsequence: PGTSGQQPSVGQQ covering amino acid residues number 2037-2049 is used, and within that subsequence the segment GTSGQ corresponding to amino acid residues 2038-2042 is more preferable. This construct has the advantage that it is know not

to be highly prone to proteolytic cleavage and is not expected to be highly immunogenic bearing in mind that fibronectin is present at high concentrations in plasma.

Human IgG_3 upper hinge based linker

The 10 amino acid residue sequence derived from the upper hinge region of murine IgG_3, PKPSTPPGSS, has been used for the production of antibodies dimerised trough a coiled coil (Pack P. and Plückthun, A. Biochemistry **31**, pp 1579-1584 (1992)) and may be useful as a spacer peptide according to the present invention. Even more preferable may be a corresponding sequence from the upper hinge region of human IgG_3. Sequences from human IgG_3 are not expected to be immunogenic in human beings.

Flexible linkers

Possible examples of flexible linker/spacer sequences include SGGTSGSTSGTGST, AGSSTGSSTGPGSTT or GGSGGAP. These sequences have been used for the linking of designed coiled coils to other protein domains (Müller, K. M., Arndt, K. M. and Alber, T., Meth. Enzymology, **328**, pp 261-281 (2000).

The linkage

The two components of the construct may be linked together by a covalent linkage. This linkage may be formed between the component X and the C or N terminal amino acid of the apo-A component. The components may also be linked via more than one covalent linkages. The covalent linkage between the components may also comprise a S-S bridge, preferably between cystein residues. These cystein residues is placed C or N terminally in the apo-A component and terminally or internally in the component X.

Carbohydrate

Irrespective of the other components of the construct the construct according to the invention may comprise a carbohydrate moiety.

Tetranectin trimerising structural element

One especially preferred embodiment of the invention is the trimerisation or partial trimerisation of an apolipoprotein or analogue thereof with the trimerisation module from tetranectin.

This technique is described in WO 98/56906 (THØGERSEN ET AL.), which is hereby incorporated by reference. The trimeric polypeptides are constructed as a monomer polypeptide construct comprising at least one tetranectin trimerising structural element (TTSE), which is covalently linked to at least one heterologous moiety. The tetranectin trimerising structural element is capable of forming a stable complex with two other tetranectin trimerising structural elements.

The term "trimerising structural element" (TTSE) used in the present description and claims is intended to refer to the portion of a polypeptide molecule of the tetranectin family which is responsible for trimerisation between monomers of the tetranectin polypeptide (SEQ ID NO 12). The term is also intended to embrace variants of a TTSE of a naturally occurring tetranectin family member, variants which have been modified in the amino acid sequence without adversely affecting, to any substantial degree, the trimerisation properties relative to those of the native tetranectin family member molecule.

Specific examples of such variants will be described in detail herein, but it is generally preferred that the TTSE is derived from human tetranectin, murine tetranectin, C-type lectin of human or bovine cartilage, or C-type lectin of shark cartilage. Especially preferred is monomer polypeptide constructs including at least one TTSE derived from human tetranectin.

The 51 residue polypeptide sequence encoded by exons 1 and 2 of tetranectin (Fig. 3, SEQ ID NO 12) appears to be unique to the tetranectin group of proteins (Fig. 4) as no significant sequence homology to other known polypeptide sequences has been established. In preparation for experimental investigations of the architecture of tetranectin a collection of recombinant proteins have been produced, the collection including complete tetranectin, the CRD domain (approximately corresponding to the polypeptide encoded by exon 3), a product corresponding to

the polypeptide encoded by exons 2+3, a product corresponding to exons 1+2 (Holtet et al., 1996). Tetranectin is indeed a trimer, but the exon 2 encoded polypeptide is in fact capable of effecting trimerisation by itself as evidenced by the observation that the recombinant protein corresponding to exons 2+3 is in fact trimeric in solution.

3D-structure analysis of crystals of full-length recombinant tetranectin (Nielsen et al., 1996; Nielsen, 1996; Larsen et al., 1996; Kastrup, 1996) has shown that the polypeptide encoded in exon 2 plus three residues encoded in exon 3 form a triple alpha helical coiled coil structure.

From the combination of sequence and structure data it becomes clear that trimerisation in tetranectin is in fact generated by a structural element (Fig. 4), comprising the amino acid residues encoded by exon two and the first three residues of exon 3 by an unusual heptad repeat sequence, that apparently is unique to tetranectin and other members of its group: This amino acid sequence (Fig. 4) is characterised by two copies of heptad repeats (abcdefg) with hydrophobic residues at a and d positions as are other alpha helical coiled coils. These two heptad repeats are in sequence followed by an unusual third copy of the heptad repeat, where glutamine 44 and glutamine 47 not only substitute the hydrophobic residues at both the a and d position, but are directly involved in the formation of the triple alpha helical coiled coil structure. These heptad repeats are additionally flanked by two half-repeats with hydrophobic residues at the d and a position, respectively.

The presence of beta-branched hydrophobic residues at a or d positions in alpha helical coiled coil are known to influence the state of oligomerisation. In the tetranectin structural element only one conserved valine (number 37) is present. At sequence position 29 in tetranectin no particular aliphatic residue appears to be preferred.

In summary, it is apparent that the triple stranded coiled coil structure in tetranectin to a large extent is governed by interactions that are unexpected in relation to those characteristic among the group of known coiled coil proteins.

The TTSEs form surprisingly stable trimeric molecules. The experimental

observations, that (1) a substantial part of the recombinant proteins exists in the oligomeric state of and can be cross-linked as trimeric molecules even at 70C° and (2) that exchange of monomers between different trimers can only be detected after exposure to elevated temperature are evidence of a extremely high stability of the tetranectin trimerising structural element. This feature must be reflected in the amino acid sequence of the structural element. In particular, the presence and position of the glutamine containing repeat in the sequential array of heptad repeats is, together with the presence and relative position of the other conserved residues in the consensus sequence (Fig. 4), considered important for the formation of these stable trimeric molecules. For most practical uses the cysteine residue 50 should be mutagenized to serine, threonine, methionine or to any other amino acid residue in order to avoid formation of an unwanted inter-chain disulphide bridge, which may lead to uncontrolled multimerisation, aggregation and precipitation of a polypeptide product harbouring this sequence.

In particular in conjunction with the trimer-stabilising exon 1 encoded polypeptide, the tetranectin trimerising structural element is a truly autonomous polypeptide module retaining its structural integrity and propensity to generate a highly stable homotrimeric complex whether it is attached or not by a peptide bond at either or at both termini to other proteins.

This unique property is demonstrated by the fact that polypeptide sequences derived from heterologous proteins may readily be trimerised when joined as fusion proteins to the tetranectin trimerising structural element. This remains valid irrespective of whether the heterologous polypeptide sequences are placed amino-terminally or carboxy-terminally to the trimerising element allowing for the formation of one molecular assembly containing up to six copies of one particular polypeptide sequence or functional entities, or the formation of one molecular assembly containing up to six different polypeptide sequences, each contributing their individual functional property.

Since three TTSEs of naturally occurring human tetranectin forms up a triple alpha helical coiled coil, it is preferred that the stable complex formed by the TTSEs of the invention also forms a triple alpha helical coiled coil.

The "tetranectin family" are polypeptides, which share the consensus sequence shown in Fig. 4 or a sequence, which is homologous at sequence level with this consensus sequence.

Hence, monomer polypeptide constructs of the invention are preferred which comprise a polypeptide sequence which has at least 68% sequence identity with the consensus sequence shown in Fig. 4, but higher sequence identities are preferred, such as at least 75%, at least 81%, at least 87%, and at least 92%.

Trip A-module

In the expression plasmids according to the present invention, the TTSE module (SEQ ID NO 12) was modified as indicated by replacing Cys 50 by Ser and including a C-terminal lysin residue. A SPGT sequence has been added to the N-terminal. This is a connective sequence to the trimerisation module. The sequence has been inserted because it gives the opportunity to cut the DNA strand with Bgl II and Kpn K. C-terminally a connective GS sequence has been added, which provides an opportunity to cut with Bam HI. This modified TTSE is designated TripA and disclosed as SEQ ID NO 13. The trimerisation module of the Apo A construct may thus advantageously comprise this sequence or a sequence haveng at least 68% sequence identity with the sequence of SEQ ID NO 13, but higher sequence identities are preferred, such as at least 75%, at least 81%, at least 87%, and at least 92%.

Specific examples of constructs encompassing the Trip A module are disclosed in the examples.

Examples of constructs according to the invention

The invention encompasses the specific sequences disclosed in the appended examples as SEQ ID NO 2 to 11 and SEQ ID NO 14. Preferably the invention encompasses SEQ ID NO 3 to 11 and SEQ ID NO 14. Sequences sharing at least 60 % sequence identity, such as at least 70 % sequence identity to these sequences are also within the scope of the invention, preferably sequences sharing

at least 80 % sequence identity, more preferably at least 90 %, more preferably at least 95 %, more preferably at least 98%.

Production of the protein construct

In order to produce a peptide component of the protein construct the cDNA encoding this part is inserted into an expression vector and transformed into a host cell.

The above mentioned host cell (which is also a part of the invention) can be prepared by traditional genetic engineering techniques which comprises inserting a nucleic acid fragment (normally a DNA fragment) encoding the polypeptide part of a monomer polypeptide construct of the invention into a suitable expression vector, transforming a suitable host cell with the vector, and culturing the host cell under conditions allowing expression of the polypeptide part of the monomer polypeptide construct. The nucleic acid fragment encoding the polypeptide may be placed under the control of a suitable promoter which may be inducible or a constitutive promoter.

Depending on the expression system, the polypeptide may be recovered from the extracellular phase, the periplasm or from the cytoplasm of the host cell.

Suitable vector systems and host cells are well-known in the art as evidenced by the vast amount of literature and materials available to the skilled person. Since the present invention also relates to the use of the nucleic acid fragments of the invention in the construction of vectors and in host cells, the following provides a general discussion relating to such use and the particular considerations in practising this aspect of the invention.

In general, of course, prokaryotes are preferred for the initial cloning of nucleic sequences of the invention and constructing the vectors useful in the invention. For example, in addition to the particular strains mentioned in the more specific disclosure below, one may mention by way of example, strains such as E. coli K12 strain 294 (ATCC No. 31446), E. coli B, and E. coli X 1776 (ATCC No. 31537). These examples are, of course, intended to be illustrative rather than limiting.

Prokaryotes are also preferred for expression, since efficient purification and protein refolding strategies are available. The aforementioned strains, as well as E. coli W3110 (F-λ, prototrophic, ATCC No. 273325), bacilli such as Bacillus subtilis, or other enterobacteriaceae such as Salmonella typhimurium or Serratia marcesans, and various Pseudomonas species may be used.

In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, E. coli is typically transformed using pBR322, a plasmid derived from an E. coli species (see, e.g., Bolivar et al., 1977). The pBR322 plasmid contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells.

The pBR plasmid, or other microbial plasmid or phage must also contain, or be modified to contain, promoters which can be used by the microorganism for expression.

Those promoters most commonly used in recombinant DNA construction include the B-lactamase (penicillinase) and lactose promoter systems (Chang et al., 1978; Itakura et al., 1977; Goeddel et al., 1979) and a tryptophan (trp) promoter system (Goeddel et al., 1979; EPO Appl. Publ. No. 0036776). While these are the most commonly used, other microbial promoters have been discovered and utilised, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally with plasmid vectors (Siebwenlist et al., 1980). Certain genes from prokaryotes may be expressed efficiently in E. coli from their own promoter sequences, precluding the need for addition of another promoter by artificial means.

In addition to prokaryotes, eukaryotic microbes, such as yeast cultures may also be used. Saccharomyces cerevisiase, or common baker's yeast is the most commonly used among eukaryotic microorganisms, although a number of other strains are commonly available. For expression in Saccharomyces, the plasmid YRp7, for

example, is commonly used (Stinchcomb et al., 1979; Kingsman et al., 1979; Tschemper et al., 1980).

This plasmid already contains the trpl gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan for example ATCC No. 44076 or PEP4-1 (Jones, 1977). The presence of the trpl lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.

Suitable promoting sequences in yeast vectors include the promoters for 3-phosphoglycerate kinase (Hitzman et al., 1980) or other glycolytic enzymes (Hess et al., 1968; Holland et al., 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. In constructing suitable expression plasmids, the termination sequences associated with these genes are also ligated into the expression vector 3' of the sequence desired to be expressed to provide polyadenylation of the mRNA and termination.

Other promoters, which have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilisation. Any plasmid vector containing a yeast compatible promoter, origin of replication and termination sequences is suitable.

In addition to microorganisms, cultures of cells derived from multicellular organisms may also be used as hosts. In principle, any such cell culture is workable, whether from vertebrate or invertebrate culture. However, interest has been greatest in vertebrate cells, and propagation of vertebrate in culture (tissue culture) has become a routine procedure (Tissue Culture, 1973). Examples of such useful host cell lines are VERO and HeLa cells, Chinese hamster ovary (CHO) cell lines, and W138, BHK, COS-7 293 and MDCK cell lines.

Expression vectors for such cells ordinarily include (if necessary) an origin of replication, a promoter located in front of the gene to be expressed, along with any necessary ribosome binding sites, RNA splice sites, polyadenylation site, and transcriptional terminator sequences.

For use in mammalian cells, the control functions on the expression vectors are often provided by viral material. For example, commonly used promoters are derived from polyoma, Adenovirus 2, and most frequently Simian Virus 40 (SV40). The early and late promoters of SV40 virus are particularly useful because both are obtained easily from the virus as a fragment which also contains the SV40 viral origin of replication (Fiers et al., 1978). Smaller or larger SV40 fragments may also be used, provided there is included the approximately 250 bp sequence extending from the HindIII site toward the BglI site located in the viral origin of replication. Further, it is also possible, and often desirable, to utilise promoter or control sequences normally associated with the desired gene sequence, provided such control sequences are compatible with the host cell systems.

An origin of replication may be provided either by construction of the vector to include an exogenous origin, such as may be derived from SV40 or other viral (e.g., Polyoma, Adeno, VSV, BPV) or may be provided by the host cell chromosomal replication mechanism. If the vector is integrated into the host cell chromosome, the latter is often sufficient.

Upon production of the polypeptide monomer constructs it may be necessary to process the polypeptides further, e.g. by introducing non-proteinaceous functions in the polypeptide, by subjecting the material to suitable refolding conditions (e.g. by using the generally applicable strategies suggested in WO 94/18227), or by cleaving off undesired peptide moieties of the monomer (e.g. expression enhancing peptide fragments which are undesired in the end product).

In the light of the above discussion, the methods for recombinantly producing the monomer polypeptide construct of the invention are also a part of the invention, as are the vectors carrying and/or being capable of replicating the nucleic acids according to the invention in a host cell or a cell-line. According to the invention the

expression vector can be e.g. a plasmid, a cosmid, a minichromosome, or a phage. Especially interesting are vectors which are integrated in the host cell/cell line genome after introduction in the host.

Another part of the invention are transformed cells (useful in the above-described methods) carrying and capable of replicating the nucleic acid fragments of the invention; the host cell can be a microorganism such as a bacterium, a yeast, or a protozoan, or a cell derived from a multicellular organism such as a fungus, an insect cell, a plant cell, or a mammalian cell. Especially interesting are cells from the bacterial species Escherichia, Bacillus and Salmonella, and a preferred bacterium is E. coli.

Yet another part of the invention relates to a stable cell line producing the polypeptide part of a construct according to the invention, and preferably the cell line carries and expresses a nucleic acid of the invention.

Receptor binding

The performance of the constructs according to the invention may be analysed by measuring the ability of the constructs to bind to receptors or HDL proteins which may bind native apolipoprotein A-I, A-II or A-IV. Such receptors and proteins include but are not limited to cubilin, megalin, Scavenger receptor class B type 1 (SR-B1), ATP-binding cassette 1 (ABC1), Lecithin:cholesterol acyltransferase (LCAT), Cholesteryl-ester transfer protein (CETP), Phospolipid transfer protein (PLTP). The dissociation constant, Kd, of the complex between cubilin and native apolipoprotein A I is 20 nM. It has been determined experimentally that an apolipoprotein A I trimer according to the present invention binds even stronger to cubilin (Figure 12).

Affinity tags

The protein construct according to the invention may also comprise an affinity tag for use during purification of the construct. Such a tag preferably comprises a polyhistidine sequence. This sequence can advantageously be used for purification of the product on a Ni^{2+} column, which will bind the polyhistidine sequence and thereby the whole protein. After elution from the column the polyhistidine sequence

may be cleaved off by a proteinase such as trombin recognising a specific sequence built into the construct between the protein construct and the polyhistidine sequence.

Other examples of affinity tags include but are not limited to well known tags such as an antigenic tag, or a GST tag. A proteolytic cleavage site may be inserted between the tag and the construct to cleave off the tag.

Signal peptides

When expressing the constructs according to the invention in E. coli or in yeast, it may be preferable to include a signal peptide in the expression construct to ensure that the expressed protein is secernated and can be harvested from the medium surrounding the cells instead of the more laborious process of isolating the expressed protein from within the cells. Specific examples of signal peptides for expression in yeast and E. coli, which can be used in conjunction with the present invention include those disclosed in WO 90/12879 (Sirtori et al), which discloses a signal peptide for expression of Apo-AI and Apo-AIM in yeast, and WO 94/13819 (Kabi Pharmacia) disclosing a signal peptide for expression of Apo-AI and Apo-AIM in E. coli.

Production of apo-A-TTSE

In order to produce a construct comprising an apolipoprotein part and a TTSE, the cDNA encoding the apolipoprotein part is ligated at the 3' end to the 5' end of the c-DNA encoding the TTSE. Further TTSE units and apolipoprotein units may also be ligated. A sequence encoding an enzyme cleavage site is further ligated to the 3' end of the sequence encoding TTSE and finally a sequence encoding polyhistidine is also ligated. This can be done by conventional PCR techniques. The combined c-DNA is inserted into an expression vector and transformed into a host cell.

After expression in the E. coli, the polyhistidine sequence is used to capture the heterologous protein on a Ni2+ column. After elution the polyhistidine tail can be removed by a proteinase such as Fx cleaving the heterologous protein at the specific site inserted into it between the TTSE and the polyhistidine sequence. The

resulting apo-A-TTSE peptide can then be processed further by trimerising it to other or identical apo-A-TTSE peptides. To improve expression in E. coli it may be advantageous to express the construct as a fusion protein together with e.g. ubiquitin, which may be cleaved off later.

Use of an apo-A construct for preparation of a pharmaceutical composition

The apo-A construct may be used for the preparation of a pharmaceutical composition. The composition may comprise pharmaceutical acceptable excipients, adjuvants, additives such as phospholipids, cholesterol, or triglycerides.

The pharmaceutical composition may be administered intravenously, intraarterially, intramusculary, transdermally, pulmonary, subcutaneously, intradermally, intratechally, through the buccal-, anal-, vaginal-, conjunctival-, or intranasal tissue, or by inoculation into tissue, such as tumour tissue, or by an implant, or orally.

The formulation of the pharmaceutical compositions according to the invention is preferably performed using techniques well known to the skilled practitioner. This may comprise the addition of pharmaceutically acceptable excipients, adjuvants, or additives, such as phospholipids, cholestorol or triglycerides.

Administration of apo-A construct

The apo-A-constructs according to the invention may be administered for prevention and/or treatment of diseases related to cholesterol, phospholipids, and triacylglycerides, LDL and HDL disorders such as hypercholesterolemia, and arteriosclerotic diseases such as atherosclerosis and myocardial infarct. Other indications include angina pectoris, plaque angina pectoris, unstable angina pectoris, arterial stenoses such as carotis stenosis, claudicatio, or cerebral arterial stenosis. Furthermore, the apolipoprotein constructs may be used for removal of endotoxins.

In one embodiment, administration comprises the administration of at least 50 mg of the construct every week such as to obtain a plasma concentration of approximately 0.5 g/L. Preferably the construct is administered parenterally such as through

injections, suppositories, implants etc. Preferably the composition is administered in an amount comprising at least 50 mg apolipoprotein construct per week, such as at least 100 mg/week, for example at least 250 mg/week, such as at least 500 mg/week, for example at least 750 mg/week such as at least 1000 mg/week, for example at least 1250 mg/week, such as at least 1500 mg/week, for example at least 2000 mg/week, such as at least 2500 mg/week, for example at least 5000 mg/week. The administration may be performed daily, every two or three days, once a week, once every second week, or once every third week, or once every fourth week.

According to another embodiment, the construct is administered once, twice or three times in much higher amounts especially for acute treatment of angina pectoris and plaque angina pectoris or unstable angina pectoris. The administration may be performed during 1, 2, 3, 4, 5, 6, 7, 8 or up to 10 days. These amounts may be at least 10 mg/kg body weight, such as at least 20 mg/kg body weight, for example at least 30 mg/kg, such as at least 40 mg/kg, for example at least 50 mg/kg, such as at least 60 mg/kg, for example at least 70 mg/kg, such as at least 75 mg/kg, for example at least 90 mg/kg, such as at least 100 mg/kg, for example at least 125 mg/kg, such as at least 150 mg/kg, for example at least 200 mg/kg, such as at least 250 mg/kg, for example at least 300 mg/kg, such as at least 400 mg/kg, for example at least 500 mg/kg, such as at least 600 mg/kg, for example at least 700 mg/kg, such as at least 800 mg/kg, for example at least 900 mg/kg, such as at least 1000 mg/kg.

The constructs may also be administered orally. For this administration route, the technology described in WO 99/46283, US 5,922,680, US 5,780,434 or US 5,591,433, US 5,609,871, or US 5,783,193 may be applied to the protein constructs according to the present invention. These references are hereby incorporated in their entirety by reference.

Cell population

The invention also encompasses the use of the nucleotide sequence according to the invention for gene therapy.

The genes may be transferred to a population of macrophages and subsequently be transferred to the patient in need of treatment. Hereby, a transient expression of the gene is obtained, since the macrophage have a limited lifetime in the blood vessels.

Permanent transfection may be obtained by transforming liver cells.

The invention is now described with specific examples of embodiments of the invention, which are to be interpreted as illustrative rather than limiting examples. The design of further constructs according to the invention lie within the normal skills of the practitioners within the art.

Example 1: Cloning of Apo A-I

The cDNA encoding Apo A-I was amplified from a human liver cDNA library (Clontech) using standard PCR techniques. For the construction of Ubi-A-I the primers used were: 5´-CAC GGA TCC ATC GAG GGT AGG GGT GGA GAT GAA CCC CCC CAG AGC-3´ and 5´- TCC AAG CTT ATT ACT GGG TGT TGA GCT TCT TAG TG-3´. The product was cloned into the vector pT7H6Ubi, described in (Ellgaard L. et al Eur. J. Biochem. 1997;244(2):544-51) using the Bam HI and Hind III cloning sites. For the construction of Trip-A-A-I the primers used were 5´-AAG GGA TCC GAT GAA CCC CCC CAG AGC CCC-3´ and 5´-TCC AAG CTT ATT ACT GGG TGT TGA GCT TCT TAG TG-3´. The PCR product was cloned into the pT7H6tripa vector described in WO 98/56906 using the Bam HI and Hind III cloning sites. For the construction of Trip-A-I-del43 the primers used were 5´-AGG GGA TCC CTA AAG CTC CTT GAC AAC TGG G-3´ and 5´- TCC AAG CTT ATT ACT GGG TGT TGA GCT TCT TAG TG -3´. The PCR product was cloned into the pT7H6tripa vector described in WO 98/56906 using the Bam HI and Hind III cloning sites. For the construction of Ubi-Cys-A-I the primers used were: 5´-GGT GGA TCC ATC GAG GGT AGG GGT GGA TGT GAT GAA CCC CCC C -3´ and 5´- TCC AAG CTT ATT ACT GGG TGT TGA GCT TCT TAG TG -3´. The product was cloned inti the vector pT7H6Ubi, described in (Ellgaard L. et al Eur. J. Biochem. 1997;244(2):544-51) using the Bam HI and Hind III cloning sites. The plasmids generated are shown on figure 4, 5, 6, and 7.

Example 2: Expression of apolipoprotein A-I (apo A-I) in *E. coli*

Ubi-A-I and Trip-A-I as well as the other constructs disclosed in the figures are conveniently expressed in *E. coli* AV-1 cells (Stratagene Inc.). Other cell lines may be used as well. Culturing of the cells and induction of expression were performed as described for tetranectin in WO 98/56906.

Example 3: Isolation and processing of protein

Crude protein was isolated by phenol extraction as described for tetranectin in WO 98/56906. The re-dissolved pellet from 6 litres of expression culture was centrifuged to remove non-dissolved material and then batch adsorbed to 50 ml Ni^{2+}-NTA-Sepharose, prepared as described in WO 98/56906. The column material was packed on a column and then washed with 500 ml 8 M urea, 500 mM NaCl, 50 mM Tris-HCl pH 8.0, then 200 ml of 6 M Guanidinium-HCl, 50 mM Tris-HCl pH 8.0 and finally 300 ml of 500 mM NaCl, 50 mM Tris-HCl pH 8.0. The protein was eluted with 500 mM NaCl, 50 mM Tris-HCl pH 8.0 and 10 mM EDTA. The protein was added 0.5 mg of Factor Xa and digested overnight at room temperature. Thrombin may be used for this purpose as well. The protein was gelfiltrated on a G-25 sephadex (Pharmacia) column in to a 500 mM NaCl, 50 mM Tris-HCl pH 8.0 buffer. Undigested protein was removed by passing the protein solution over a Ni^{2+}-NTA-Sepharose column pre-washed in 500 mM NaCl, 50 mM Tris-HCl pH 8.0 and then washed with 500 mM NaCl, 50 mM Tris-HCl pH 8.0. Undigested protein was eluted with 500 mM NaCl, 50 mM Tris-HCl pH 8.0 and 10 mM EDTA. Further purification may be performed using Sp Sepharose ion exchange.

Example 4: Removal of lipids from the proteins

The proteins were gelfiltrated into a 10 mM $(NH_4)_2CO_3$ pH 8.8 solution and lyophilised. The lyophilised protein was resuspended in 25 ml cold 1:1 methanol/chloroform, incubated on ice for 30 min, centrifuged at 3000 *g* for 20 minutes. The pellet was resuspended in 25 ml of 1:2 cold methanol/chloroform, equilibrated for 30 minutes on ice and recentrifuged. The supernatant was removed and the pellet was briefly air-dried and then redissolved in 6 M guanidinium-HCl, 50 mM Tris-HCl pH 8.0 over night.

Example 5: Multimerisation assay

Cross linking

Multimerisation may be measured by cross-linking of multimers followed by analytical SDS-PAGE.

60 µl of a 0.2 mg/ml protein dissolved in 150 mM Na-borate pH 9.0 equillibrated to the desired temperature for 30 minutes are added 5 µl of a 20 mg/ml dimethylsuberimidate and incubated for 30 minutes at the desired temperature. The cross-linking was quenched by the addition of 5 µl 3 M Tris-HCl pH 9.0.

Dimethylsuberimidate causes lysin residues located within a short distance from one another to form a covalent bond. The result is that proteins which have formed multimers are covalently linked to one another. The molecular weight of the multimers can be estimated in the subsequent SDS-PAGE.

The cross-linking products were analysed by SDS-PAGE on 8-16 % polyacrylamide gels. Optionally an adjuvant, such as a lipid, was included in the cross-linking mixture, in which case the protein was pre-incubated with the adjuvant.

Analytical gelfiltration

Multimerisation may also be measured by analytical gelfiltration.

The protein was dissolved in a 500 mM NaCl, 50 mM Tris-HCl pH 8.0 buffer and gelfiltrated on a Superdex 200 HR 10/30 column in to the desired buffer at room temperature and a flow of 0.25 ml/min. For standard procedures the buffer was 100 mM NaCl, 50 mM Tris-HCl pH 8.0.

From Figure 13 it can be seen that Apo A-I elutes as composite peaks, the major ones centred at approximately 14.5 and 16.5 mL. BSA, with a molecular weight of 68 kDa, elutes at approximately 14.5 ml, indicating that the Apo A-I peak at 16.5 ml corresponds to monomeric Apo A-I, while the other major peak corresponds to apo A-I self-association complexes. The constructs fused to the trimerisation domain all

elute with a main peak at approximately 10.7 ml and a minor peak at 14 ml. The peak at 14 ml probably corresponds to the trimeric form of the constructs, while the main peak at 10.7 ml corresponds to a high molecular weight product. Presumably the product is formed by association of the trimers. This indicates that fusion of apo A-I to the trimerisation domain does not only lead to trimers, but also to the formation of large complexes, where the Apo A-I units can interact with other apo A-I units, like native apo A-I can interact with other Apo A-I molecules.

Example 6: Kinetics of association of the protein construct with dimyristoyl phosphatidylcholine (DMPC)

The ability of the constructs according to the invention to bind to a lipid can conveniently be measured using a well known assay such as the association to dimyristoyl phosphatidylcholine (DPMC).

The assay was conducted as described in (Bergeron J. et al. (1997), Biochem. Biophys. Acta, 1344, 139-152. Dried DPMC was suspended in 100 mM NaCl, 50 mM Tris-HCl pH 8.0 and 0.25 mM EDTA above its transition temparature at a concentration of 0.5 mg/ml. The protein sample, buffer and the DMPC suspension were all incubated at 24 °C 10 minutes, and then mixed so that the final concentration of DMPC became 0.4 mg/ml, with a protein conc. of 5.2 μM (of the monomer). The reduction in turbidity of the mixture, reflecting increasing lipid-protein association, was followed by measuring the absorbance of the mixture at 325 nm. The assay was conducted four times each for apo AI, Trip-A-AI and Trip-A-FN-AI, and one time without adding protein.

From Figure 11 it can be seen that all Apo A-I constructs bind DMPC. For all the three constructs tested the turbidity was totally cleared after 24 hours, indicating that the capacity of the fusion proteins to bind DMPC is present in the fusion proteins. However, apparently both Trip-A-Apo A-I and Trip-A-FN-Apo AI binds DMPC slower than does native Apo A-I at 24°C, which is the only temperature at which the assay is functional.

Example 7: Surface plasmon resonance analysis of the binding of the derivatives to cubilin

The assay was conducted as described in: Kozyraki R, Fyfe J, Kristiansen M, Gerdes C, Jacobsen C, Cui S et al. The intrinsic factor-vitamin B12 receptor, cubilin, is a high-affinity apolipoprotein A-I receptor facilitating endocytosis of high-density lipoprotein. Nat Med 1999; 5(6):656-661.. The concentration of apolipoprotein construct used was 0.5 µM. Results (Figure 12) are only shown for TripA-AI and apo A-I. Binding similar to that observed for TripA-AI was observed for TripA-FN-AI and TripA-TN-AI. The response increased upon trimerisation of apo A-I, especially there was a decrease in the of-rate, based on the gained "avidity" of the interaction for a multimer with an immobilised target compared to a monomer (bonus of multivalency). Showing that apo A-I was able to bind cubilin in the trimeric state, and that more than one apo A-I was in a conformation capable of interacting with cubilin, indicating correct folding of the apo A-I unit in the trimeric construct.

Example 8: Evaluation of the plasma clearance of apolipoprotein A-I, TripA Apo-A-I and TripA fibronectin-linker Apo-A-I in mice.

Three groups of five mice each were each injected 1 mg of apo A-I, Trip-A-AI or Trip-A-FN-AI, respectively. The protein was dissolved at a concentration of 0.33 mg/ml in the following buffer: 1 x PBS pH 7.4, and 8.9 mg/ml dipalmitoylphosphatidylcholine. Blood samples were taken from each mice at the following times after the injection: 10 min., 4 h, 24 h, and 48 h.

The plasma concentrations of apolipoprotein A-I and derivatives were measured using an ELISA assay as follows:

Nunc Immuno PolySorp plates were used, each vial was added 100 µL in each addition. MB corresponds to the following buffer composition: 2 mM $CaCl_2$, 1 mM $MgCl_2$, 10 mM HEPES, 140 mM NaCl.

Plates were coated overnight in cold-room with 4 µg/ml of polyclonal anti-human apo A-I from rabbit (DAKO A/S) dissolved in 50 mM$NaHCO_3$ pH 9.6. Plates were

washed in MB + 0.05 % Tween-20 pH 7.8 and blocked in MB + 0.05 % Tween-20 + 1 % BSA pH 7.8 for 1 hour. The sample was applied dissolved in MB + 0.05 % Tween-20 + 1 % BSA pH 7.8 and incubated for 1 hour, washed in MB + 0.05 % Tween-20 + 1 % BSA pH 7.8 and incubated for 1 hour with monoclonal anti-apo A-I from mice (PerImmune Inc, clone 10-A8) at a concentration of 1 µg/ml in MB + 0.05 % Tween-20 + 1 % BSA pH 7.8. Plates were washed and incubated with a secondary anti-mice IgG antibody linked to horse radish peroxidase. Plates were washed again and developed using OPD-tablets and H_2O_2, the reaction was stopped using 1 M H_2SO_4. The result was compared to a standard based on known concentrations of apo A-I and derivatives, respectively. No effect of diluting Apo A-I in mice plasma was observed for the standard.

The results, shown in figure 14, verify that the plasma clearance time of the construct Trip A Apo A-I is increased at least 3 times compared to the clearance time of native Apo AI. Preliminary data indicate that the clearance time for Trip A FN Apo A-I is at least the same as for Trip A Apo A-I. These data together with the cubilin binding data and DMPC binding data document that the constructs according to the invention are strong candidates for treating the diseases mentioned in the present application.

Example 9 Plasmids

The construct according to the invention may be manufactured using the plasmids disclosed below.

Insertion of a linker sequence in Trip-A-AI

The basic linker containing constructs, with the mutations mentioned, was constructed as was the construct with-out linker. I.e. by PCR amplification of Apo A-I (and the linker sequence) and insertion into the pT7FxH6-Trip-A plasmid. The reverse primer was the same as used for the construction of pT7H6FxTrip-A-AI, while the forward primers used were:

pT7H6FX-Trip-A-FN(-2)-AI:

5´-CGC GGATCC TCG GGT CA**G** GAT GAA CCC CCC CAG AGC CCC –3'

Unfortunately all the isolated clones had the above highlighted **G** mutated to a T, indicating a faulty sequence of the primer.

pT7H6FX-Trip-A-TN-AI-Bam-S

5'- cgc gga tcc aag gtg cac atg aag gat gaa ccc ccc cag agc ccc-3'

The mutations mentioned was corrected by site directed mutagenesis using the QuickChange kit from Stratagene and the following sets of primers:

pT7H6FX-Trip-FN-AI:
5'-acg gtc tcc ctg aag gga acc tcg ggt cag gat g-3'
5'-cat cct gac ccg agg ttc cct tca ggg aga ccg t-3'

pT7H6FX-Trip-A-TN-AI
5'-acg gtc tcc ctg aag gga acc aag gtg cac atg aag g-3'
5'-cct tca tgt gca cct tgg ttc cct tca ggg aga ccg t-3'

Removal of the heparin-binding site of Trip-A

As a further derivation of the constructs, the heparin binding site of the Trip-A sequence (Lorentsen RH, Graversen JH, et al. Biochemical Journal (2000), 347 pp 83-87, was mutated using the site directed mutagenseis kit from Stratagene and the following set of primers:

For the mutation of lysine 9 from Trip-A:
5'-cca acc cag aag ccc aag gcg aat gta aat gcc-3'
5'-gtg ttc aca aca tct gcc ttg gca ttt aca atc-3'

For the mutation of lysine 15 from Trip-A:

5'-ggc att tac aat cgc ctt ggg ctt ctg ggt tgg-3'
5'-cca acc cag aag ccc aag gcg att gta aat gcc-3'

These mutations are planned to be made on all the relevant Trip-A-apo-AI derivatives, possibly them all. Generating double mutants K9A, K15A of the trip-A derivatives, named TripA-FN-AI-K9AK15A, TripA-TN-AI-K9AK15A and TripA-AI-K9AK15A.

Furthermore truncation of the N-terminal could also remove the heparin affinity without removing the trimerisation. See Holtet et al. Protein Science (1997), Lorentsen et al. Biochem. Journal (2000), Nielsen et al. FEBS (1997) and Nielsen et al Acta Cryst D. (2000). The N-terminal residue would then preferably be located between Val 16 and Met 22.

Construction of the expression plasmid for Hp-α-A-I

First the plasmid pT7H6Fx-Hp(alpha) (Figure 10H) was constructed as follows:

From a cDNA library (Clontech fetal liver) the Hp-alpha sequence was PCR amplified using the following set of primers:
Non-sense primer: 5'-cac aag ctt tcc gct aga tct ctg cac tgg gtt agc cgg att ctt ggg -3'
Sense Primer: 5'-ggt gga tcc atc gag ggt agg ggt gtg gac tca ggc aat gat gtc acg g-3' - 3'

The PCR product contained the flowing features:

BamH I- site- Hp alpha sequence – Bgl II site –Hind III site.

In the Hp-alpha sequence the cystein disulfide bridging with the beta-chain of Hp was mutated to an alanine.

The product was digested with BamH I and Hind III and inserted into the pT7H6FX plasmid, which was sequenced. A PCR product encoding human Apo AI was made using the standard non-sense primer also used for making pT7H6-Ubi-Fx-ApoAI and pT7H6Fx-TripA-AI. While the sense primer used was the one used as sense primer in the construction of pT7H6FX-TripA-AI. Giving a PCR product with the following features:

BamH I site – Apo AI sequence – Hind III site, this product was digested with BamH I and Hind III and inserted into the above mentioned plasmid digested with Bgl II and Hind III. The resulting plasmid pT7H6FX-Hp(alpha)-Apo AI was sequenced and expression tested in E. coli.

pT7H6 TripA-apoAI (Figure 7):

The plasmid comprises the plasmid pT7H6FxtripA described in WO 98/56906 as example no. 1.

Expression is governed by the T7 promoter. The plasmid furthermore comprises a H6 sequence being a hexa-His affinity tag for use in purification. After that is inserted a Factor Xa recognition sequence (IQGR).

-SPGT is a connective sequence to the subsequent trimerisation module. This sequence has been inserted because it gives the opportunity to cut the DNA strand with Bgl II and Kpn I.

–Trip A is the trimerisation module from tetranectin..

GS is another connective sequence, which provides an opportunity to cut with Bam. HI.

Finally the plasmid comprises the human apoliprotein A-I cDNA coding for amino acids 25 -267 from human apolipoprotein A-I. The expressed and purified protein corresponds to SEQ ID NO 3.

pT7H6TripA-apoA1-del43 (Figure 8):

The plasmid comprises the sequences as above, but the apolipoprotein part has been replaced with cDNA coding for amino acids 68-267 from human apolipoprotein A-I. The expressed and purified protein corresponds to SEQ ID NO 4.

pT7H6UbiFxApoAI (Figure 5):

The basic plasmid has been described in Ellgaard et al (1997).

The plasmid comprises the following sequences:

- the expression is governed by the T7 promoter

-H6: hexa-His affinity tag for purification of the protein construct

-Ubi: cDNA coding for human ubiquitin inserted to stabilise the protein in E. coli.

-FX: recognition sequence for Factor Xa
-DNA coding for two Gly residues, necessary for the optimal cleavage by Factor Xa.
-ApoAI: cDNA coding for amino acids 25 -267 from human apolipoprotein A-I
The expressed and purified protein corresponds to SEQ ID NO 1.

pT7H6UbiFXCysApoAI (Figure 6):

As above, but after the sequence coding for the two glycine residues and before the apolipoprotein A-I sequence coding for a cystein residue has been inserted. The expressed and purified protein corresponds to SEQ ID NO 2.

PT7H6FXCysApoAI (Figure 9):

The plasmid comprises the following sequences:
- the expression is governed by the T7 promoter
-H6: hexa-His affinity tag for purification of the protein construct
-FX: recognition sequence for Factor Xa
-DNA coding for two Gly residues, necessary for the optimal cleavage by Factor Xa.
-DNA coding for a cystein residue.
-ApoAI: cDNA coding for amino acids 25 -267 from human apolipoprotein A-I
The expressed and purified protein corresponds to SEQ ID NO 2.

Further examples of plasmids for expression of apolipoprotein constructs according to the invention are disclosed in Figure 10 A to G together with the corresponding amino acid sequences of the expressed and purified proteins, which are disclosed in the sequence listing.

REFERENCES

Bergeron et al 1997, Biochem Biophys Acta, 1344:139-152.

Bolivar et al, 1977. Gene, 2: 95.

Chang et al. 1978. Nature, 275: 617-624.

Ellgaard et al (1997). Dissection of the domain architecture of the $\alpha_2$macroglobulin-receptor-associated protein. Eur J Biochem vol 244:544-551.

Fiers et al. 1978. Nature, 273: 113.

Goeddel et al. 1979. Nature, 281: 544.

Hess et al. 1969. Advances in Enzyme Regulation, 7: 149-166.

Hitzman et al. 1980. Journal of Biological Chemistry, 25: 12073-12080.

Holland et al. 1978. Biochemistry, 17: 4900.

Holtet, T.L., Graversen, J.H., Thøgersen, H.C. and Etzerodt, M. (1996).Domains and shared motifs in plasminogen - ligand interaction. Poster 21st Annual Lorne Conference on Protein Structure and Function, held Melbourne, Australia, February 4-8, 1996.

Itakura et al. 1977. Science, 198: 1056.

Jones. 1977. Genetics, 85: 23-33.

Kastrup, J.S. (1996). Lecture at Minisymposium held by EU HCM contract CHRX-CT93-0143: Protein Crystallography I in Hamburg, Germany, December 13-14, 1996.

Kingsman et al, 1979, Gene :141.

Larsen, I.K., Nielsen, B.B., Rasmussen, H. and Kastrup, J.S. (1996). Poster, 17th International Crystallography Congress, Seattle, USA held August 8-17. 1996.

Neame, P.J. and Boynton, R.E. (1996). Protein Soc. Symposium, (Meeting date 1995; 9th Meeting: Tech. Prot. Chem VII). Proceedings pp. 401-407 (Ed., Marshak, D.R.; Publisher: Academic, San Diego, Calif.).

Nielsen, B.B. (1996). Lecture, Lundbeck Centre Neuro-Medicinal Chemistry Minisymposium held November 5, 1996 at the Royal Danish School of Pharmacy, Copenhagen.

Nielsen, B.B., Larsen, I.K., Rasmussen, H. and Kastrup, J.S. (1996). Lecture, Danish Crystallographer's Meeting, held June 3-4, 1996 at the Royal Danish School of Pharmacy, Copenhagen.

Siebwenlist et al. 1980. Cell, 20: 269.

Sørensen et al, 1995, Gene, 152:243-245.

Stinchomb et al. 1979. Nature 282: 39.

Tschemper et al. 1980. Gene, 10: 157.